

SEQUENCE LISTING

<110> Mitsuhashi, Tadayoshi

<120> METHODS FOR DETERMINING GENETIC RESISTANCE OF PIGS
TO DISEASES CAUSED BY RNA VIRUSES

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<150> JP 2002-313076

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<170> PatentIn Ver. 2.1

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<222> (101)..(2092)

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Met Val Tyr Ser Ser
1 5

tgt gaa agt aaa gaa cct gat tca gtt tct gca tcc aat cac ctg tta 163
Cys Glu Ser Lys Glu Pro Asp Ser Val Ser Ala Ser Asn His Leu Leu
10 15 20

cta aat ggg aat gat gaa ttg gtg gag aaa agt cac aaa aca ggg cct 211
Leu Asn Gly Asn Asp Glu Leu Val Glu Lys Ser His Lys Thr Gly Pro
25 30 35

gag aac aac ctg tac agc cag tac gag gag aaa gtg cgg ccc tgc atc 259
Glu Asn Asn Leu Tyr Ser Gln Tyr Glu Glu Lys Val Arg Pro Cys Ile
40 45 50

gac ctc atc gac tca ctg cgg gcc ctg ggc gtg gag cag gac ctg gcc	307
Asp Leu Ile Asp Ser Leu Arg Ala Leu Gly Val Glu Gln Asp Leu Ala	
55 60 65	
ctg ccc gcc atc gcc gtc atc ggg gac cag agt tcg ggc aag agc tcc	355
Leu Pro Ala Ile Ala Val Ile Gly Asp Gln Ser Ser Gly Lys Ser Ser	
70 75 80 85	
gtg ctg gag gcc ctg tcg ggg gtc gct ctc ccc aga ggc agc gga att	403
Val Leu Glu Ala Leu Ser Gly Val Ala Leu Pro Arg Gly Ser Gly Ile	
90 95 100	
gtg aca aga tgc cct ctt gtg ctg aaa ttg aaa aaa ctc gtg aac gaa	451
Val Thr Arg Cys Pro Leu Val Leu Lys Leu Lys Lys Leu Val Asn Glu	
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Glu Asp Glu Trp Lys Gly Lys Val Ser Tyr Arg Asp Ser Glu Ile Glu	
120 125 130	
ctt tca gat gct tcg cag gtg gaa aag gaa gtc agc gca gcc cag att	547
Leu Ser Asp Ala Ser Gln Val Glu Lys Glu Val Ser Ala Ala Gln Ile	
135 140 145	
gcc atc gct ggg gaa ggc gtg gga atc agt cat gag cta atc agt ctg	595
Ala Ile Ala Gly Glu Gly Val Gly Ile Ser His Glu Leu Ile Ser Leu	
150 155 160 165	
gag gtc agc tcc cct cat gtc cca gat ctg acc ctc ata gac ctt cct	643
Glu Val Ser Ser Pro His Val Pro Asp Leu Thr Leu Ile Asp Leu Pro	
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ggc atc acc agg gta gct gta ggc aat cag cca tac gac atc gaa tac	691
Gly Ile Thr Arg Val Ala Val Gly Asn Gln Pro Tyr Asp Ile Glu Tyr	
185 190 195	
cag atc aag tct ctg atc aag aag tac atc tgt aag cag gag acc atc	739
Gln Ile Lys Ser Leu Ile Lys Lys Tyr Ile Cys Lys Gln Glu Thr Ile	
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aac ttg gtg gtg gtc ccc tgt aac gtg gac att gcc acc acg gag gcg	787
Asn Leu Val Val Val Pro Cys Asn Val Asp Ile Ala Thr Thr Glu Ala	
215 220 225	
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Leu Arg Met Ala Gln Glu Val Asp Pro Glu Gly Asp Arg Thr Ile Gly	
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atc ttg acg aag ccg gat ctg gtg gac aaa ggc act gag gac aag ata	883
Ile Leu Thr Lys Pro Asp Leu Val Asp Lys Gly Thr Glu Asp Lys Ile	
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Val Asp Val Ala Arg Asn Leu Val Phe His Leu Lys Lys Gly Tyr Met	

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gcc aag gcc ctg cag aag gag cag gcc ttc ttt gaa aac cac gca cat Ala Lys Ala Leu Gln Lys Glu Gln Ala Phe Phe Glu Asn His Ala His 295 300 305			1027
ttc agg gat ctt ctg gag gaa ggg cgg gcc acg atc ccc tgc ctg gca Phe Arg Asp Leu Leu Glu Glu Gly Arg Ala Thr Ile Pro Cys Leu Ala 310 315 320 325			1075
gaa aga ctg acc tct gaa ctc atc atg cac atc tgt aaa act ctg ccc Glu Arg Leu Thr Ser Glu Leu Ile Met His Ile Cys Lys Thr Leu Pro 330 335 340			1123
ctg tta gaa aac caa ata aaa gag agt cac cag aaa ata aca gag gag Leu Leu Glu Asn Gln Ile Lys Glu Ser His Gln Lys Ile Thr Glu Glu 345 350 355			1171
tta cag aag tat ggc tcc gat att cca gag gat gaa agc ggg aag atg Leu Gln Lys Tyr Gly Ser Asp Ile Pro Glu Asp Glu Ser Gly Lys Met 360 365 370			1219
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aat ttc aaa aat ggt tat gac gcc ata tgt aaa caa atc cag ctc ttc Asn Phe Lys Asn Gly Tyr Asp Ala Ile Cys Lys Gln Ile Gln Leu Phe 425 430 435			1411
gaa aat cag tac agg ggg aga gag ttg cca ggg ttt gtg aat tat aag Glu Asn Gln Tyr Arg Gly Arg Glu Leu Pro Gly Phe Val Asn Tyr Lys 440 445 450			1459
aca ttt gaa acc atc att aag aag cag gtc agt gtc ctg gaa gag cca Thr Phe Glu Thr Ile Ile Lys Lys Gln Val Ser Val Leu Glu Glu Pro 455 460 465			1507
gcc gtg gac atg ctg cac aca gtg act gat tta gtc cgg ctc gcc ttc Ala Val Asp Met Leu His Thr Val Thr Asp Leu Val Arg Leu Ala Phe 470 475 480 485			1555

aca gat gtt tca gaa aca aat ttt aat gaa ttt ttc aac ctc cac aga 1603
 Thr Asp Val Ser Glu Thr Asn Phe Asn Glu Phe Phe Asn Leu His Arg
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act gcc aag tcc aaa att gaa gac att aaa tta gaa caa gaa aaa gaa 1651
 Thr Ala Lys Ser Lys Ile Glu Asp Ile Lys Leu Glu Gln Glu Lys Glu
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gct gag acg tcg atc cgg ctc cac ttc caa atg gag cag atc gtg tac 1699
 Ala Glu Thr Ser Ile Arg Leu His Phe Gln Met Glu Gln Ile Val Tyr
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 Cys Gln Asp Gln Val Tyr Arg Gly Ala Leu Gln Lys Val Arg Glu Lys
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 Ser Pro Ala Pro Ser Ser Asp Pro Ser Ile Ala Glu Ile Phe Gln His
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ctg att gcc tac cat cag gag gtc ggc aag cgc atc tcc agc cac atc 1891
 Leu Ile Ala Tyr His Gln Glu Val Gly Lys Arg Ile Ser Ser His Ile
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 Pro Leu Ile Ile Gln Phe Phe Ile Leu Arg Thr Phe Gly Gln Gln Leu
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 Gln Lys Ser Met Leu Gln Leu Leu Gln Asn Lys Asp Gln Tyr Asp Trp
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ctc ctg agg gag cgc agt gac acc agc gac aag agg aag ttc ctg aag 2035
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 Glu Arg Leu Met Arg Leu Thr Gln Ala Arg Arg Arg Leu Ala Lys Phe
 650 655 660

cca ggc tga accggactct ccaggcggcc cggggtctcc agggcacgtc 2132
 Pro Gly

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cacatcctcc tgtggttagt agactctaaa gccaccgtcc ctgctgttag tggctgagga 2252

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 His Lys Thr Gly Pro Glu Asn Asn Leu Tyr Ser Gln Tyr Glu Glu Lys
 35 40 45
 Val Arg Pro Cys Ile Asp Leu Ile Asp Ser Leu Arg Ala Leu Gly Val
 50 55 60
 Glu Gln Asp Leu Ala Leu Pro Ala Ile Ala Val Ile Gly Asp Gln Ser
 65 70 75 80
 Ser Gly Lys Ser Ser Val Leu Glu Ala Leu Ser Gly Val Ala Leu Pro
 85 90 95
 Arg Gly Ser Gly Ile Val Thr Arg Cys Pro Leu Val Leu Lys Leu Lys
 100 105 110
 Lys Leu Val Asn Glu Glu Asp Glu Trp Lys Gly Lys Val Ser Tyr Arg
 115 120 125
 Asp Ser Glu Ile Glu Leu Ser Asp Ala Ser Gln Val Glu Lys Glu Val
 130 135 140
 Ser Ala Ala Gln Ile Ala Ile Ala Gly Glu Gly Val Gly Ile Ser His
 145 150 155 160
 Glu Leu Ile Ser Leu Glu Val Ser Ser Pro His Val Pro Asp Leu Thr
 165 170 175
 Leu Ile Asp Leu Pro Gly Ile Thr Arg Val Ala Val Gly Asn Gln Pro
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 Tyr Asp Ile Glu Tyr Gln Ile Lys Ser Leu Ile Lys Lys Tyr Ile Cys
 195 200 205
 Lys Gln Glu Thr Ile Asn Leu Val Val Val Pro Cys Asn Val Asp Ile

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Thr Glu Asp Lys Ile Val Asp Val Ala Arg Asn Leu Val Phe His Leu 260 265 270		
Lys Lys Gly Tyr Met Ile Val Lys Cys Arg Gly Gln Gln Asp Ile Gln 275 280 285		
Glu Gln Leu Ser Leu Ala Lys Ala Leu Gln Lys Glu Gln Ala Phe Phe 290 295 300		
Glu Asn His Ala His Phe Arg Asp Leu Leu Glu Glu Gly Arg Ala Thr 305 310 315 320		
Ile Pro Cys Leu Ala Glu Arg Leu Thr Ser Glu Leu Ile Met His Ile 325 330 335		
Cys Lys Thr Leu Pro Leu Leu Glu Asn Gln Ile Lys Glu Ser His Gln 340 345 350		
Lys Ile Thr Glu Glu Leu Gln Lys Tyr Gly Ser Asp Ile Pro Glu Asp 355 360 365		
Glu Ser Gly Lys Met Phe Phe Leu Ile Asp Lys Ile Asp Ala Phe Asn 370 375 380		
Ser Asp Ile Thr Ala Leu Ile Gln Gly Glu Glu Leu Val Val Glu Tyr 385 390 395 400		
Glu Cys Arg Leu Phe Thr Lys Met Arg Asn Glu Phe Cys Arg Trp Ser 405 410 415		
Ala Val Val Glu Lys Asn Phe Lys Asn Gly Tyr Asp Ala Ile Cys Lys 420 425 430		
Gln Ile Gln Leu Phe Glu Asn Gln Tyr Arg Gly Arg Glu Leu Pro Gly 435 440 445		
Phe Val Asn Tyr Lys Thr Phe Glu Thr Ile Ile Lys Lys Gln Val Ser 450 455 460		
Val Leu Glu Glu Pro Ala Val Asp Met Leu His Thr Val Thr Asp Leu 465 470 475 480		
Val Arg Leu Ala Phe Thr Asp Val Ser Glu Thr Asn Phe Asn Glu Phe 485 490 495		
Phe Asn Leu His Arg Thr Ala Lys Ser Lys Ile Glu Asp Ile Lys Leu		

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Glu Gln Glu Lys Glu Ala Glu Thr Ser Ile Arg Leu His Phe Gln Met 515	520	525
Glu Gln Ile Val Tyr Cys Gln Asp Gln Val Tyr Arg Gly Ala Leu Gln 530	535	540
Lys Val Arg Glu Lys Glu Ala Glu Glu Glu Lys Asn Arg Lys Ser Asn 545	550	555 560
Gln Tyr Phe Leu Ser Ser Pro Ala Pro Ser Ser Asp Pro Ser Ile Ala 565	570	575
Glu Ile Phe Gln His Leu Ile Ala Tyr His Gln Glu Val Gly Lys Arg 580	585	590
Ile Ser Ser His Ile Pro Leu Ile Ile Gln Phe Phe Ile Leu Arg Thr 595	600	605
Phe Gly Gln Gln Leu Gln Lys Ser Met Leu Gln Leu Leu Gln Asn Lys 610	615	620
Asp Gln Tyr Asp Trp Leu Leu Arg Glu Arg Ser Asp Thr Ser Asp Lys 625	630	635 640
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ctccaggcgg cccggggtct ccagggcacg tctccaggca acgaggacca acctccttcc 180